# Is There a Critical Target Gene for the First Step in Carcinogenesis?

by Ann R. Kennedy\*

Our work has suggested that a high-frequency event is involved in the initiation phase of malignant transformation in vitro; a later, mutationlike event appears to be involved in the later stages of transformation. There may be no specific "target gene" which directly interacts with carcinogens. It is hypothesized that nonspecific types of DNA damage are involved in the induction of an ongoing process we know as carcinogenesis. Several genes could be involved in maintaining this process. Our recent results suggest that c-myc and c-fos could be involved in the early stages of carcinogenesis, as they are affected by anticarcinogenic protease inhibitors in a manner that corresponds to the way in which protease inhibitors suppress malignant transformation.

## Nature of the Initiating Event in Carcinogenesis

Our previous work has suggested that a high-frequency event is involved in the induction of radiation-induced transformation  $in\ vitro\ (1-8)$ . The work of several other investigators has now suggested that a similar high-frequency initiating event occurs in carcinogenesis in both  $in\ vitro\$ and  $in\ vivo\$ systems, with many different types of DNA-damaging agents initiating the carcinogenic process, as has been reviewed elsewhere (7-11).

Given the high-frequency nature of the initiating event in carcinogenesis, it is unlikely to be a specific locus mutation, as studies of mutation frequencies have shown them to occur at orders of magnitude below those observed for malignant transformation. The initiating event does not behave like a mutation, as it appears to be a reversible phenomenon. We have observed that certain protease inhibitors, which are highly effective in their ability to suppress malignant transformation in vitro (12) and in vivo (13), are capable of reversing initiation (14). There is much evidence from in vivo studies that lesions thought to represent "initiated" or "premalignant" cells are capable of reverting to their normal state. For example, Terzaghi-Howe (15) observed that contact with normal tracheal epithelium could revert initiated "pre-neoplastic" tracheal epithelial cells to a normal condition. It is well known that "premalignant" lesions in vivo, such as squamous metaplasia, dysplasia, etc., are readily reversible in nature.

The nature of the high-frequency initiating event is unknown. Several radiation/carcinogen-induced processes that could be involved in carcinogenesis and are likely explanations for our observations have been discussed elsewhere (1-8). There are many possibilities for the initiating event in carcinogenesis. For example, carcinogens such as radiation have been shown to alter DNA methylation patterns in a widespread fashion (16). Methylation of DNA is thought to play an important role in gene regulation; we have hypothesized that the initiating event in carcinogenesis involves altered gene expression (1-8). Another event that is induced in a widespread fashion in a population of mammalian cells by a number of different carcinogens (including radiation) is gene amplification (17-19). It is of interest to us that modifiers of carcinogenesis also affect the level of gene amplification; for example, gene amplification can be potentiated by tumor-promoting agents such as 12-O-tetradecanoylphorbol-13-acetate (TPA) (19) and inhibited by agents that suppress carcinogenesis, such as certain protease inhibitors known to have anticarcinogenic activity (20). The nature of the initiating event in carcinogenesis deserves much more intensive study.

#### Target Genes in Carcinogenesis

Several genes are likely to be involved in maintenance of the ongoing process induced by carcinogens. Two genes are of particular interest to us in that their expression is affected by the anticarcinogenic protease inhibitors in a manner which corresponds to the way in which the protease inhibitors affect the induction of transformation *in vitro*; these genes are c-myc (21-24) and c-fos (25). Protease inhibitors affect the expression of these genes as summarized in Table 1. As the anti-

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Table 1. Suppression of gene expression by protease inhibitors.

Protease inhibitor	Ability of protease inhibitors to suppress:				
		c-myc expression			
	Actin expression	Nontransformed cells	Transformed cells	c-fos expression	Radiation-induced transformation
Bowman-Birk	<del>-</del>	+ +	_	+++	+++
Antipain	_	+ + +	_	++	++
Leupeptin	$\mathrm{ND}^{b}$	+ +	ND	ND	++
$\alpha_1$ -antitrypsin	ND	-	ND	~~	_
Elastatinal	ND	_	ND	ND	_
Soybean trypsin inhibitor	ND		ND	ND	-

<sup>&</sup>lt;sup>a</sup>In terms of effective molar concentrations of protease inhibitors.

carcinogenic protease inhibitors are not capable of affecting c-myc expression in transformed cells but do affect c-myc in nontransformed cells, our results suggest that c-myc regulation may be of great importance in the malignant transformation of cells, as discussed in detail elsewhere (24).

We have hypothesized that the anticarcinogenic protease inhibitor effects on c-myc expression and malignant transformation are involved in an early stage of carcinogenesis, even though protease inhibitors can affect carcinogenesis at long time periods after carcinogen exposure (14). Our proposed scheme for the induction of malignant transformation in vitro is shown in Figure 1.

Carcinogens such as radiation are known to induce c-myc; we have shown that c-myc is induced in vivo by radiation and that anticarcinogenic protease inhibitors reduce c-myc expression to normal levels (26). It has also been shown that c-myc expression is elevated in radiation-induced tumors (27). As shown in Figure 1, it is expected that anticarcinogenic protease inhibitors reduce c-myc expression to normal levels after carcinogen exposure; this phenomenon has been shown to occur in the irradiated mouse colon (26). It is possible that elevated c-myc expression influences the level of expression of another gene—specifically, as shown in Figure 1, a gene coding for a particular protease, the Boc-Val-

Pro-Arg-MCA hydrolyzing activity, which has been studied extensively in our laboratory (13,28-30).

The c-muc gene codes for a nuclear binding protein and is thought to play a regulatory role in gene transcription (31). Our research would suggest that there must be persistent activation of the process involved in malignant transformation. While c-myc is only transiently activated by radiation (26), the Boc-Val-Pro-Arg-MCA hydrolyzing activity is persistently activated by carcinogen exposure (30). We have observed higher than normal levels of Boc-Val-Pro-Arg-MCA hydrolyzing activity in normal-appearing areas of carcinogentreated epithelial cells in vivo, even at long time periods after carcinogen exposure (30). This proteolytic activity is directly affected by the anticarcinogenic protease inhibitors in a manner that corresponds to the way in which these agents suppress malignant transformation in vitro (13,28) and in vivo (13,30). As shown in Figure 1, it is proposed that c-myc induction precedes the induction of the protease (Boc-Val-Pro-Arg-MCA hydrolyzing activity). It is perhaps equally likely that the order of these two phenomena is reversed, as it is known that proteases such as plasminogen activator induce cmyc expression. Many other agents studied in carcinogenesis research induce c-myc expression; for example, TPA is known to induce c-myc gene expression (32).

We have hypothesized that a late event is involved

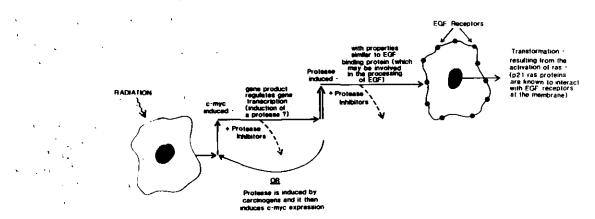


FIGURE 1. Our hypothesized scheme for events involved in radiation transformation in vitro. Anticarcinogenic protease inhibitors have been shown to affect both c-myc and a specific proteolytic activity (the Boc-Val-Pro-Arg-MCA hydrolyzing activity), as described in the text.

<sup>&</sup>lt;sup>b</sup>ND, not determined.

in actually transforming a cell to the malignant state (1-8,12). In Figure 1, we have hypothesized that the activation of ras is involved in a late stage of carcinogenesis. There are several ways in which an interaction between the events we believe are related to the early stages of carcinogenesis (i.e., the induction of c-myc and the induction of a protease such as the Boc-Val-Pro-Arg-MCA hydrolyzing activity) and members of the ras gene family could occur. Cooperation between myc and ras in the induction of transformation is well documented (33,34). The Boc-Val-Pro-Arg-MCA hydrolyzing activity has characteristics that make it likely to be involved in the processing of a growth factor like epidermal growth factor (EGF) (13,28). If this proteolytic activity were involved in the processing of a growth factor like EGF, more of an EGF-like substance would be present than under normal conditions. Carcinogentreated cells growing under the influence of abnormally large amounts of a growth factor would be likely to exhibit altered growth characteristics; such altered growth patterns are known to occur in a widespread fashion in carcinogen-treated tissue (and are known as premalignant changes). We propose that an additional change occurs in these atypical areas and that it is this later change that leads directly to malignancy; the evidence for such a late step in the malignant transformation of C3H10T1/2 cells and carcinogenesis in vivo has been reviewed (1-8,12). We propose here that this later change involves the activation of ras, which occurs as a late event in several in vitro systems (e.g., 35) and is known to be activated in many different kinds of cancers, including those induced by radiation (36,37). It is possible that the activation of ras is connected to the cellular effects brought about by EGF, as it is known that the p21 proteins of ras interact with the EGF re-

ceptor (the product of c-Ha-ras is activated by EGF) (38). Although the Boc-Val-Pro-Arg-MCA hydrolyzing activity we have studied has characteristics similar to EGF binding protein (28), which is thought to be involved in the processing of EGF, it is not exactly like EGF binding protein. Thus, we have hypothesized that a growth factor involved in the malignant transformation of cells in the systems we have used may be similar to EGF.

There is some evidence to suggest that a growth factor like EGF is involved in the induction of transformation in vitro; for example, EGF is known to promote transformation in vitro (39), and it is known that EGF as a promoting agent can bring about an irreversible change in cells (such as a point mutation in ras that leads to its activation), that is, the switch to anchorage-independent growth (which correlates with tumorigenicity) in promotable cells (40).

### Protease Inhibitor Suppression of cmyc Gene Expression

The mechanism by which anticarcinogenic protease inhibitors suppress c-myc gene expression is unknown, although many hypotheses have been presented elsewhere (21-24). A potential model for c-myc gene expression and its regulation by a protease is shown in Figure 2. Our model proposes that a protease is capable of destroying a regulatory protein involved in the regulation of c-myc; this regulatory protein would conceivably bind to the promoter region of the gene, as shown in Figure 2. Carcinogens could increase the level of the protease, which would lead to decreased levels of the regulatory protein; decreased binding of the regulatory

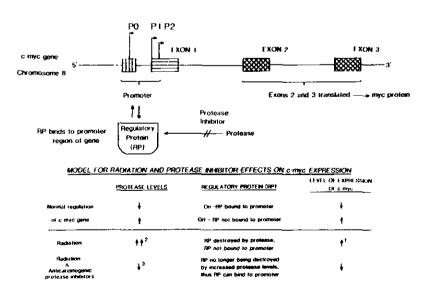


FIGURE 2. Proposed model to explain c-myc gene expression and its regulation by a protease. It is hypothesized that anticarcinogenic protease inhibitors operate in our proposed model as described in the text. (1-3) Evidence in support of proposed model: c-myc expression increases in radiation-induced tumors in vivo protease levels increase in carcinogen-treated tissue in vivo (30), anticarcinogenic protease inhibitors return protease levels to normal (30).

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protein to the promoter region of c-myc would then lead to increased levels of c-myc gene expression. Evidence in support of this part of the proposed model comes from experiments showing that: a) carcinogens induce elevated levels of a protease: Boc-Val-Pro-Arg-MCA hydrolyzing activity (13,28); b) radiation increases c-myc gene expression (26); and c) c-myc gene expression increases in radiation-induced tumors in vivo (27).

Conceivably, anticarcinogenic protease inhibitors could then inhibit the protease that destroys the regulatory protein. In fact, anticarcinogenic protease inhibitors have been shown to inhibit carcinogen-induced protease activity, the Boc-Val-Pro-Arg-MCA hydrolyzing activity, in vivo (30), and in vitro (13,28), as well as radiation-induced c-myc levels in vivo (26).

We are currently attempting to determine whether the schematic presentation in Figure 2 is actually occurring during the regulation of c-myc expression by protease inhibitors. Current hypotheses for the mechanism of regulation of the c-myc gene are described in detail elsewhere (23,24). While the exact characteristics of the regulatory protein hypothesized to be involved in c-muc gene regulation are unknown. Zajac-Kave et al. (41) have described a DNA-binding activity that binds to the 5' region of the first intron of c-muc; this binding activity is thought to be intimately involved in c-muc gene regulation. We are performing experiments to determine whether alterations in the levels or other changes in this DNA-binding activity can explain our observations on protease inhibitors and c-myc gene expression as they relate to carcinogenesis.

Although the models of carcinogenesis presented here are highly speculative, the anticarcinogenic protease inhibitor effects on the suppression of c-myc and c-fos gene expression and the Boc-Val-Pro-Arg-MCA hydrolyzing activity are well documented. It is believed that the effects of those agents that modify carcinogenesis on specific genes may lead us to an understanding of the role these genes play in the carcinogenic process.

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